

30

35

40

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq SXXCFVSVPPASA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

```

Met Ala Ser Ser Ser Pro Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val
      -20                      -15                      -10

Ser Val Pro Pro Ala Ser Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn
      -5                      1                      5

Ser Asp Xaa Pro Arg Asp Glu Val Gln Glu Val Val Phe Val Pro Ala
      10                      15                      20                      25

Gly Thr His Thr Pro Gly Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val
      30                      35                      40

Glu Gln Val Ser Lys Thr His Ala Val Ile Leu Ser Arg Pro Ser Trp
      45                      50                      55

Leu Trp Gly Ala Glu Met Gly Xaa Thr Ser Met Val Ser Ala Leu Ala
      60                      65                      70

Thr Arg Leu Cys Gly Arg Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu
      75                      80                      85

Leu Gly Met Asp Leu Leu Arg Cys Arg Pro Cys
      90                      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -39..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq XLIAXLEPPGAMA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

```

Met Xaa Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met
    -35                      -30                      -25

Ala Pro Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu
    -20                      -15                      -10

Glu Pro Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
    -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq PMLGLAAFRWIWS/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

```

Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg Pro Asn Ser
-45                      -40                      -35                      -30

Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val
    -25                      -20                      -15

Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser
    -10                      -5                      1

Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala
    5                      10                      15

```

Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Xaa
20 25 30 35
Asn Arg Arg Ala Val
40

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq AALCSLFFFLSLQ/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu
-15 -10 -5
Ser Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala
 -45 -40 -35

Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu
 -30 -25 -20

Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe
 -15 -10 -5 1

Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LLLLVHSFWFTVC/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln Ser Ile Ala
 -35 -30 -25

Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Val His Ser
 -20 -15 -10

Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LFCVLLSLRPHTS/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gln Asn Phe Cys His His Leu Ala Ile Cys Thr Val Ile Leu Phe
 -25 -20 -15

Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser Gly Thr Leu Trp Ala
 -10 -5 1 5

Ser Ser Ala His Gly Leu His Leu Ala Pro Ala Glu Pro Gln Leu Ser
 10 15 20

Cys Trp Met Cys Cys Ala
 25

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Pro Ser Phe Ser Lys Asp Leu Leu Thr Val Pro Lys Leu Gly Thr
 -60 -55 -50

Gly His Xaa Xaa Gly Xaa Gly Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu
 -45 -40 -35

Leu Lys Cys Leu Trp Ser Asn Val Val Pro Glu Cys Thr Met Ala Ser
 -30 -25 -20

Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala
 -15 -10 -5

Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp Leu

1 5 10 15
Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp
 20 25 30
Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Xaa Xaa Lys Phe Pro
 35 40 45
Lys Leu Xaa Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val Asp
 50 55 60
Gln Glu Leu Ile Glu Asp Xaa
 65 70

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq LEMXAFASHXA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala
-20 -15 -10
-
Ser His Ile Xaa Ala Arg Asp Ala Ala Gly Ser Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -139..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq FGLLHQLSQCVTS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```

Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser Ala Ser
      -135                -130                -125

Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly Gly Val
      -120                -115                -110

Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala Ala Ala
      -105                -100                -95

Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe Glu Asn
      -90                  -85                -80

Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg Arg Val
      -75                -70                -65                -60

Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr Asp Glu
      -55                -50                -45

Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu Leu Ile
      -40                -35                -30

Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys Phe Gly
      -25                -20                -15

Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu
      -10                -5                1
  
```

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -43..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.1
 seq SAATLASLGGTSS/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Lys Glu Leu Glu Arg Gln Gln Lys Glu Val Glu Glu Arg Pro Glu
-40 -35 -30

Lys Asp Phe Thr Glu Lys Gly Ser Arg Asn Met Pro Gly Leu Ser Ala
-25 -20 -15

Ala Thr Leu Ala Ser Leu Gly Gly Thr Ser Ser Arg Arg Gly Ser Gly
-10 -5 1 5

Asp Thr Ser Ile Ser Ile Asp Pro Glu
10

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq VLVILCIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile Val
-20 -15 -10

Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala Glu
-5 - 1 5 10

Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr Ala
15 20 25

Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr Lys
30 35 40

Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala Val
45 50 55

Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile
60 65 70

(2) INFORMATION FOR SEQ ID NO: 518:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -70..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

```

Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa Glu Ser
-70                               -65                               -55

Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala Cys His
                               -50                               -45                               -40

Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln
                               -35                               -30                               -25

Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu
                               -20                               -15                               -10

Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Xaa
                               -5                               1                               5                               10

Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa Ile Val
                               15                               20                               25

Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln
                               30                               35                               40

Glu

```

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu
-20 -15 -10

Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -73..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
-70 -65 -60

Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
--55 -50 -45

Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
-40 -35 -30

Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
-25 -20 -15 -10

Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
-5 1 5

Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
10 15 20

Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
25 30 35

Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
40 45 50

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LGAAALALLANT/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu
  -20                      -15                      -10

Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys
   -5                      1                      5

Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys
  10                      15                      20                      25

Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala
   30                      35                      40

Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu
   45                      50                      55

Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val
   60                      65                      70

Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
  75                      80

```

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

```

Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp Asp Ile Glu Arg
-30                      -25                      -20

Gly Arg Leu Pro Leu Leu Leu Val Ala Asn Ala Gly Thr Ala Ala Val
-15                      -10                      -5                      1

Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu Cys Glu Gln Tyr
                    5                      10                      15

Gly Ile Trp Leu His Val Glu Gly Val Asn
                20                      25

```

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15                      -10                      -5

Val Trp
1

```

(2) INFORMATION FOR SEQ ID NO: 524:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -33..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.8
seq FICLQWALPHSEA/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

Met Asn Ala Gln Pro Gly Leu Xaa Leu Asp Cys Ile Thr Arg Phe Leu
      -30                -25                -20

Thr Xaa Gly Gln Phe Ile Cys Leu Gln Trp Ala Leu Pro His Ser Glu
      -15                -10                -5

Ala Gly Asp Phe Glu Ala Lys
  1                5

```

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -69..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq LCRLCLVRLFCC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

```

Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
      -65                -60                -55

Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val
      -50                -45                -40

Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe
      -35                -30                -25

Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val

```

-20

-15

-10

Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq AALLLTATVRLSA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser Leu Trp
-25 -20 -15
Ala Ala Leu Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser Pro Gly
-10 -5 1

Pro

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LLFFGKLLVVGG/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -91..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq SVLELIVASVCQS/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile Lys Glu Gly Asp
-90 -85 -80

Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val Trp Glu Pro Arg
-75 -70 -65 -60

Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala Tyr Pro Val Glu
-55 -50 -45

Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu Glu Ile Arg Lys
 -40 -35 -30

His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro Val Thr Ser Val
 -25 -20 -15

Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His Ile Arg Thr Thr
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LYMLAEALPVSHG/AH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu Leu Asp Arg Leu
 -65 -60 -55

Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val Arg Arg Val Phe
 -50 -45 -40 -35

Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe Met Glu Val Glu
 -30 -25 -20

Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala Leu Pro Val Ser
 -15 -10 -5

His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala Ser Ala Leu Gln
 1 5 10

Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser Gly
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq IIFLIQWHGSVFQ/EF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Leu Leu Gly Thr Ser Asn Ile Ile Ile Phe Leu Ile Gln Trp His
-20 -15 -10

Gly Ser Val Phe Gln Glu Phe
-5 1

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -20...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6
seq AFVXACVLSLIST/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa Ala Cys Val Leu Ser
-20 -15 -10 -5

Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp
1 5 10

Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys
15 20 25

Ser Ile Trp Asp Glu Leu
30

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq MSLTSGFLRVSQG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
    -10                      -5                      1

Leu Ser Gln
    5

```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq AIRTLSVTGILA/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile
    -60                      -55                      -50

Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His
    -45                      -40                      -35

```

Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val
 -30 -25 -20

Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu
 -15 -10 -5 1

Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His
 5 10 15

Trp Ile Lys Leu Met Asn
 20

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq AGLLEFGSLAGLGA/YQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly
 -50 -45 -40

Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala
 -35 -30 -25

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala
 -20 -15 -10 -5

Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val
 1 5 10

Phe Leu Ala Thr Ser Gly Thr Leu Ala
 15 20

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq CCALLTSLXCIWG/PA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr
-35                -30                -25                -20

Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa Cys
          -15                -10                -5

Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
          1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -42..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
-40                -35                -30

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
-25                -20                -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
-10                -5                1                5

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
          10                15                20

```

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LSVSLLPCAGAWS/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
 -65 -60 -55

Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
 -50 -45 -40

Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
 -35 -30 -25 -20

Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
 -15 -10 -5

Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
 1 5 10

Ser Ile Leu Xaa Thr Val Val Val Ile
 15 20

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq LLMLGVTLPNYSYW/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly
      -25                      -20                      -15

Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser
      -10                      -5                      1

Thr Val His Gly Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu
      5                      10                      15

Trp Phe Ser Ser Ala Gly
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq XFLXLXXLSXXWP/XD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser
-20                      -15                      -10                      -5

Xaa Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp
      1                      5                      10

Thr Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
      15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -67..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq LILERPLVPSAEA/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```

Met His Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala
  -65                      -60                      -55

Arg Gly His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala
  -50                      -45                      -40

Pro Ala Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp
 -35                      -30                      -25                      -20

Glu Thr Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser
      -15                      -10                      -5

Ala Glu Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu
      1                      5                      10

Ser Asn Tyr Ala Leu
  15

```

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.9
seq GLWLALVDGLVRX/AP

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Met Ala Gly Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu
-40 -35 -30
Ser Gln Ile Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu
-25 -20 -15
Trp Leu Ala Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile
-10 -5 1 5
Xaa Gly

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -78..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq VGAVFGLITCISA/HV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
-75 -70 -65
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
-60 -55 -50
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
-45 -40 -35
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
-30 -25 -20 -15
Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
-10 -5 1
Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg
5 10

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLQVLPVILLLLG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -15 -10 -5

Leu Gly Val Pro Pro Ser
 1

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LLILDMNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala Ala
 -35 -30 -25

Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn Val
 -20 -15 -10

Leu Tyr Thr Asp Ala Ser Pro Leu Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VLLAIGMFFTAWF/FV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe Pro His Leu
 -30 -25 -20

Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala Trp Phe Phe
 -15 -10 -5 1

Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile Tyr Lys Glu
 5 10 15

Leu Gln

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LMLSSSLPLLIWL/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

```

Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr Leu Phe
-35          -30          -25          -20

Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro Leu Leu
          -15          -10          -5

Ile Trp Leu Lys Asp Arg
          1

```

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

```

Met Leu Glu His Leu Xaa Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly
          -35          -30          -25

Gln Lys Leu Ala Xaa Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala
          -20          -15          -10

Ile Val Gly Phe Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr
          -5          1          5

Val Tyr Ile Val Met Ala Gly
10          15

```

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SKVLFCFSNVLG/FD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly
-15 -10 -5

Phe Asp Tyr
1

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
-25 -20 -15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
-10 -5 1 5

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
10 15 20

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Ser Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LGLALGRLEGGSA/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

```

Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
  -50                -45                -40

Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
  -35                -30                -25

Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
  -20                -15                -10                -5

Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
          1                5                10

Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro
  15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LIALTCLDGTTVS/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

```

Met Asn Ala Leu Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala

```

-25 -20 -15
 Leu Thr Cys Leu Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met
 -10 -5 1 5
 Thr Met Gly Cys Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met
 10 15 20
 Ser Val Gly Pro Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser
 25 30 35
 Ile Trp Met Ala Asp Met Ile Xaa Asp
 40 45

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLVYLVTAERVWS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 -45 -40 -35 -30
 Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 -25 -20 -15
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 -10 -5 1
 Lys

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq SLFIYIFXTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser Asn Thr
-15                      -10                      -5

Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1              5              10              15

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
      20              25              30

Cys Phe Xaa Leu Gln
      35

```

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LNSLSALAE LAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

```

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15                      -10                      -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
 1              5              10              15

```

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp
-15 -10 -5
Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr
1 5 10 15
Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val
20 25

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Leu Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile
-20 -15 -10
Leu Cys Val Ser Val Lys Ala Gly Ser Thr
-5 1

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LQFVLPVATQIQQ/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met Gly Lys Met Leu
-25 -20 -15

Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln Glu Val Ile Lys
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LCALGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Ser Pro Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro
-20 -15 -10

Ser Ser Met Trp Ala Gly Glu
-5 1

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq MTOLLSASPWALT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Thr Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser
-10 -5 1

Ser Glu Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu
5 10 15

Ser Gln Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu
20 25 30 35

Cys Phe Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val
40 45 50

Ala Thr Gly His Xaa
55

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2

Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr Ser Leu Thr Cys
-25 -20 -15

Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys Ser Met Ala Thr
-10 -5 1 5

Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg Pro Pro Arg Lys
10 15 20

Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly Val Val Leu Cys
25 30 35

Thr Phe Thr Arg Asn Arg
40

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1

seq LEAFSQAISAIQA/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln
-20 -15 -10

Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe
-5 1 5

Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg
10 15 20 25

Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn
30 35 40

Arg Asp Pro

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

```

Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His
  -30                      -25                      -20

Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn
  -15                      -10                      -5

Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr
   1                      5                      10                      15

His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser
      20                      25                      30

Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq ACLAWTAVRPSAC/CH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser Ala Cys
 -15 -10 -5

Cys His Pro Gln Ser Ala Asn Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VFGMSSSSGASNS/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
 -55 -50 -45 -40

Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
 -35 -30 -25

Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
 -20 -15 -10

Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
 -5 1 5

Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -15...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq FFLFLSFVLMYDG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

```
Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp Gly
-15                      -10                      -5

Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr Met
1              5              10              15

Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
20              25              30
```

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -27...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq SIKVLLQSALSGLG/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

```
Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25                      -20                      -15

Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10                      -5              1              5

Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10              15              20
```

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

```

Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu Leu Ala Phe Val Glu
  -15                      -10                      -5

Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
   1                      5                      10                      15

Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
                20                      25                      30

Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Xaa
                35                      40                      45

Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Xaa Met Met
   50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq SLIPLFXFIGTGA/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

```

Met Leu Arg Gln Ile Ile Gly Gln Ala Lys Lys His Pro Ser Leu Ile
  -25                      -20                      -15

```

Pro Leu Phe Xaa Phe Ile Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr
 -10 -5 1 5

Leu Leu Arg Leu Ala Leu Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa
 10 15 20

Asn Pro Glu Pro Trp Asn Xaa Leu Gly Pro Glu
 25 30

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -98..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq WTSLTCSLVVVDG/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Val Lys Glu Thr Gln Tyr Tyr Asp Ile Leu Gly Val Lys Pro Ser
 -95 -90 -85

Ala Ser Pro Glu Arg Ser Arg Arg Pro Ile Gly Ser Trp Arg Ser Ser
 -80 -75 -70

Thr Thr Arg Thr Arg Thr Arg Met Arg Ala Arg Ser Leu Asn Ser Tyr
 -65 -60 -55

Pro Arg His Met Lys Cys Phe Gln Ile Gln Arg Lys Gly Met Phe Met
 -50 -45 -40 -35

Thr Lys Ala Glu Ser Arg Gln Xaa Lys Lys Glu Ala Gln Ala Ala Pro
 -30 -25 -20

Ala Ser Leu His Pro Trp Thr Ser Leu Thr Cys Ser Leu Val Val Val
 -15 -10 -5

Asp Gly Cys Gly
 1

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

```

Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu
-35                -30                -25

Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly
-20                -15                -10                -5

Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val
          1                5                10

Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu
    15                20                25

Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr
    30                35                40

Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro
    45                50                55                60

Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala
          65                70                75

Gln

```

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq RIELCQRSPGSQG/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

```

Met Ala Ala Ala Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu
  -30                -25                -20

Arg Xaa Ile Arg Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly
  -15                -10                -5

Val Arg Asp Phe Ile
  1                5
  
```

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
 (B) TYPE: AMINO ACID
 (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -44..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IALTLPMSLSRA/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

```

Met Phe Pro Ser Cys Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu
  -40                -35                -30

Leu Ser Ile Phe Ser Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile
  -25                -20                -15

Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys
  -10                -5                1

Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys
  5                10                15                20

Gly
  
```

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -60..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq QLXFLYFVCCIFQ/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala Tyr
-60 -55 -50 -45

Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile Gly
-40 -35 -30

Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala Gln
-25 -20 -15

Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr Tyr
-10 -5 1

Xaa
5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq SSCSCSLISFTRG/DK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Met Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile
-20 -15 -10

Ser Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe
 -5 1 5 10

Leu Val Tyr Asn Ala Asp Gln
 15

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq SILGIISVPLSIG/YC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg
 -60 -55 -50

Xaa Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys
 -45 -40 -35

Val Leu Pro His Met Ile Glu Arg Lys Xaa Xaa Lys Ile Val Thr Val
 -30 -25 -20 -15

Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys
 -10 -5 1

Ala Ser Xaa His Ala Leu Xaa Gly Phe Phe Asn Xaa Leu Arg Thr Xaa
 5 10 15

Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -98..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LALRTSWISSVCS/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

```

Met Gly Gly Ser Gly Ser Arg Leu Ser Lys Glu Leu Leu Ala Glu Tyr
      -95                      -90                      -35

Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu Ile Leu Leu Ala His Arg
      -80                      -75                      -70

Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Xaa Xaa Ser Arg His
      -65                      -60                      -55

Phe Gly His Lys Cys Pro Ser Ser Arg Phe Ser Ala Phe Gln Ser Ser
      -50                      -45                      -40                      -35

Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala Gly Ser Ser Pro His Pro
      -30                      -25                      -20

Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr Ser Trp Ile Ser Ser Val
      -15                      -10                      -5

Cys Ser Val Thr Gln Pro Arg Gln Thr Ser Ser Pro Ile Met Pro Ser
      1                      5                      10

Ala Ser Leu Thr Leu Met Met Thr
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

```

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
    -25                      -20                      -15

Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
    -10                      -5                      1

Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro Glu Lys Pro
    5                      10                      15                      20

Lys Leu Leu

```

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -114..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ATFVTQALIQXYA/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

```

Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys Lys
    -110                      -105                      -100

Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala Glu
    -95                      -90                      -85

Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys Cys
    -80                      -75                      -70

Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu Ala
    -65                      -60                      -55

Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu Pro
    -50                      -45                      -40                      -35

Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu Ala
    -30                      -25                      -20

For Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln Xaa
    -15                      -10                      -5

Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp
    1                      5

```

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq TCSVCCYLFWLIA/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
-55 -50 -45 -40

Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
-35 -30 -25

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
-20 -15 -10

Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
-5 1

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -58..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq GGILMGSFQGTIA/GQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

```

Met Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His
-55 -50 -45

Ser Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu
-40 -35 -30

Ile Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile
-25 -20 -15

Leu Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala
-10 -5 1 5

Thr Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly
10 15 20

Ala Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser
25 30 35

His Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly
40 45 50

Val Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala
55 60 65 70

```

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWWCFHLQAEASA/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

```

Met Gly Trp Gln Arg Trp Trp Cys Phe His Leu Gln Ala Gln Ala Ser
-15 -10 -5

Ala His Pro Pro Gln Gly Leu Gln
1 5

```

(2) INFORMATION FOR SEQ ID NO: 582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq VIFFACVVRVRDG/LP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

```

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly Leu
-15                -10                -5                1

Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu Glu
      5                10                15

Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys
    20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq TALAAXTWLGVNG/VR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

```

Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp Gly
-15                -10                -5

Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu Asn
  1                5                10                15

```

Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe Gly
20 25 30
Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
35 40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12
seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
-15 -10 -5
Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
1 5 10
Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
15 20 25 30
Ser Ala Met Tyr Cys Asp Glu Leu
35

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 -15 -10 -5
 Ser Gly Gln Tyr Tyr Asp Trp
 1 5

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12
 seq FTLFLALIGGTSG/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 -15 -10 -5
 Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
 1 5 10
 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
 15 20 25 30
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
 35 40 45
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
 50 55 60
 Ile Asp Gln Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Gly
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.9
seq LLLLLLPFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

```

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
-20          -15          -10          -5

Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
          1          5          10

Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
          15          20          25

Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
          30          35          40

Gly Ala Arg Val Tyr Xaa Ala Xaa Xaa Asp Val Glu Lys Gly Glu Leu
          45          50          55          60

Val Ala Xaa Glu Ile Gln Thr Thr Thr Gly Xaa Xaa Gln Val Leu Val
          65          70          75

Arg Xaa Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala
          80          85          90

```

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1

seq LLYLLVPALFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala Gly
 -15 -10 -5 1

Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser Pro
 5 10 15

Leu Phe Pro Lys Pro Tyr Pro Asn Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Met Lys Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu
 -30 -25 -20

Phe Pro Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro
 -15 -10 -5

Ala Asn Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln
 1 5 10 15

Thr Gln Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg
 20 25 30

Ala Val Ser Pro Pro Ala Lys
 35

(2) INFORMATION FOR SEQ ID NO: 590:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.9
seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Met Leu Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys
-15 -10 -5
Ser Gln Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly
1 5 10 15
Tyr Glu Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys
20 25 30
Asp Ile Val Pro Asp Ala Cys Lys Gly Gly Met Lys Cys Val Asn His
35 40 45
Tyr Gly Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn
50 55 60
Asn Glu Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly
65 70 75
Ala Thr Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val
80 85 90 95
Leu Xaa Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro
100 105 110
Glu Met Gln Thr Gly Arg Asn Asn Phe Val
115 120

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: AMINO ACID

(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq LLILWFHLCVSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

```

Met Glu Lys Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His
  -20                      -15                      -10

Leu Asp Cys Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser
  -5                      1                      5                      10

Leu His Val Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro
                15                      20                      25

Ser Ser Asn Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys
                30                      35                      40

Ser Pro Glu Ala Val
                45
  
```

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

```

Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
-15                      -10                      -5                      1

Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
                5                      10                      15

Gly Arg Ala Gly Gly
                20
  
```

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq LLFVATLPFWTHY/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu Tyr Asp Asp
-90 -85 -80 -75

Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe Gly Thr Val
-70 -65 -60

Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly Leu Val Gly
-55 -50 -45

Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys Pro Lys Ser
-40 -35 -30

Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp Leu Leu Phe
-25 -20 -15

Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn Glu Lys Gly
-10 -5 1 5

Leu His Asn Ala Met Cys
- 10

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47, C12N 15/10, 15/11		A3	(11) International Publication Number: WO 99/06550 (43) International Publication Date: 11 February 1999 (11.02.99)
(21) International Application Number: PCT/IB98/01232 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,144 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).			(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report</i> (88) Date of publication of the international search report: 29 April 1999 (29.04.99)
(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN PROSTATE			
(57) Abstract <p>The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be used to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.</p>			

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01232

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 C12N15/10 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL - EMBEST16 Entry MMAA66264, Acc.No. AA166264, 21 December 1996 MARRA, M. ET AL.: "ms49f10.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone 614923 5'." XP002083641 see the whole document	3-7
X	DATABASE EMBL - EMHUM2 Entry HSPEX, Acc.No. Y10196, 6 February 1997 FRANCIS, F. ET AL.: "H. sapiens PEX gene" XP002083642 nt. 174570-174600 --- -/-	3,8

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Date of the actual completion of the international search

10 November 1998

Date of mailing of the international search report

17.02.99

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Authorized officer

Smalt, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01232

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	ADAMS M D ET AL: "INITIAL ASSESSMENT OF HUMAN GENE DIVERSITY AND EXPRESSION PATTERNS BASED UPON 83 MILLION NUCLEOTIDES OF CDNA SEQUENCE" NATURE, vol. 377, no. SUPPL, 28 September 1995, pages 3-17, XP002069461 see table 12	
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A	--- DATABASE EMBL - EMEST8 Entry HS1301911, Acc.No. AA506459, 4 July 1997 STRAUSBERG, R.: "nh46a08.s1 NCI CGAP Pr5 Homo sapiens cDNA clone IMAGE:955382 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN)." XP002083802 see abstract	
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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/TB 98/01232

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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A	LOCKHART D J ET AL: "EXPRESSION MONITORING BY HYBRIDIZATION TO HIGH-DENSITY OLIGONUCLEOTIDE ARRAYS" BIO/TECHNOLOGY, vol. 14, no. 13, December 1996, pages 1675-1680, XP002022521 see the whole document ---	35-37
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A	KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application ---	
A	EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application ---	
A	CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application ---	
A	WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 ---	
A	TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204 ---	
A	YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 ---	
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 98/01232

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-37 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:316, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

2. Claims: Invention 2-278: claims 1-37 all partially

Inventions 2-278: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-315, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 317, invention 3 is limited to Seq.ID:40 and 318,....., invention 278 is limited to Seq.ID:315 and 593).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 98/01232

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